

H12



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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/554,960**

**DATE: 06/30/2004**  
**TIME: 13:03:05**

**Input Set : A:\Nih342-1.app**  
**Output Set: N:\CRF4\06302004\I554960.raw**

3 <110> APPLICANT: Kaslow, David C.  
 4 Tsuboi, Takafumi  
 5 Torii, Motomi  
 6 The Government of the United States of America  
 7 as represented by the Secretary of the  
 8 Department of Health and Human Services  
 10 <120> TITLE OF INVENTION: Vaccines for Blocking Transmission of Plasmodium vivax  
 12 <130> FILE REFERENCE: 015280-34210US  
 14 <140> CURRENT APPLICATION NUMBER: US 09/554,960  
 C--> 15 <141> CURRENT FILING DATE: 2000-05-22  
 17 <150> PRIOR APPLICATION NUMBER: US 60/045,283  
 18 <151> PRIOR FILING DATE: 1997-05-01  
 20 <150> PRIOR APPLICATION NUMBER: WO PCT/US98/25742  
 21 <151> PRIOR FILING DATE: 1998-12-04  
 23 <160> NUMBER OF SEQ ID NOS: 24  
 25 <170> SOFTWARE: PatentIn Ver. 2.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1066  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Plasmodium vivax  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (147)..(857)  
 35 <223> OTHER INFORMATION: Pvs28  
 37 <400> SEQUENCE: 1  
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 40 ttatacaaaa acgactcccc ctttgagata acacccaact gagctcgatt cccctccccc 120  
 42 acttttgcgc ctcccccttg ttcaaa atg aat acc tac cac agc ttg ctg ttc 173  
 43 Met Asn Thr Tyr His Ser Leu Leu Phe  
 44 1 5  
 46 ctt ctg gcc atc gtg ctt act gtt aag cac acc ttc gca aag gtc acc 221  
 47 Leu Leu Ala Ile Val Leu Thr Val Lys His Thr Phe Ala Lys Val Thr  
 48 10 15 20 25  
 50 gcg gag acc caa tgc aaa aat ggc tat gta gtc caa atg agc aat cat 269  
 51 Ala Glu Thr Gln Cys Lys Asn Gly Tyr Val Val Gln Met Ser Asn His  
 52 30 35 40  
 54 ttt gaa tgc aaa tgc aac gac ggg ttt gtt atg gca aat gaa aac act 317  
 55 Phe Glu Cys Lys Cys Asn Asp Gly Phe Val Met Ala Asn Glu Asn Thr  
 56 45 50 55  
 58 tgc gag gaa aaa cgc gat tgc aca aat cca caa aat gta aat aaa aac 365  
 59 Cys Glu Glu Lys Arg Asp Cys Thr Asn Pro Gln Asn Val Asn Lys Asn  
 60 60 65 70  
 62 tgt gga gac tac gct gtg tgt gca aac acc aga atg aat gat gag gaa 413

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63 Cys Gly Asp Tyr Ala Val Cys Ala Asn Thr Arg Met Asn Asp Glu Glu
64      75          80          85
66 aga gca tta cga tgc ggc tgc ata tta ggg tac acc gta atg aat gag      461
67 Arg Ala Leu Arg Cys Gly Cys Ile Leu Gly Tyr Thr Val Met Asn Glu
68   90          95          100          105
70 gtg tgt act cca aat aaa tgt aac ggc gtt ttg tgt gga aag gga aag      509
71 Val Cys Thr Pro Asn Lys Cys Asn Gly Val Leu Cys Gly Lys Gly Lys
72           110         115         120
74 tgc atc tta gat ccc gct aat gtg aac agc acc atg tgc tct tgt aat      557
75 Cys Ile Leu Asp Pro Ala Asn Val Asn Ser Thr Met Cys Ser Cys Asn
76           125         130         135
78 ata gga acc aca ttg gat gaa tct aaa aaa tgt gga aag cca gga aaa      605
79 Ile Gly Thr Thr Leu Asp Glu Ser Lys Lys Cys Gly Lys Pro Gly Lys
80           140         145         150
82 act gaa tgc acg ttg aag tgt aag gca aac gaa gaa tgt aaa gag act      653
83 Thr Glu Cys Thr Leu Lys Cys Lys Ala Asn Glu Glu Cys Lys Glu Thr
84           155         160         165
86 cag aat tat tac aag tgc gtt gcg aag gga agc ggc gga gaa ggc agc      701
87 Gln Asn Tyr Tyr Lys Cys Val Ala Lys Gly Ser Gly Gly Glu Gly Ser
88   170         175         180         185
90 ggt gga gaa ggc agc ggc gga gag ggc agc ggc gga gag ggc agc ggc      749
91 Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly
92           190         195         200
94 gga gag ggc agc ggt gga gac aca gga gca gct tac agt ctc atg aac      797
95 Gly Glu Gly Ser Gly Gly Asp Thr Gly Ala Ala Tyr Ser Leu Met Asn
96           205         210         215
98 gga tct gca gta atc agc ata cta ctt gta ttc gcc ttc ttc atg atg      845
99 Gly Ser Ala Val Ile Ser Ile Leu Leu Val Phe Ala Phe Phe Met Met
100          220         225         230
102 tca tta gtg tagacgattc tacacacaca cacaacata cacaaggggga      894
103 Ser Leu Val
104          235
106 gaagcgtctc acagagtcat ttcaagtcat acgcacaaaa aaggaaagta catccagctg 954
108 gtgaaaagagc atttatgtgt gcagttatcc ttgggagaag caccctccac ccagttgcgt 1014
110 tgctgttacc ttaaaactta gtggcaccca tatcgaattt gactttgctc gc      1066
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114 <211> LENGTH: 236
115 <212> TYPE: PRT
116 <213> ORGANISM: Plasmodium vivax
118 <400> SEQUENCE: 2
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122 Val Lys His Thr Phe Ala Lys Val Thr Ala Glu Thr Gln Cys Lys Asn
123   20         25          30
125 Gly Tyr Val Val Gln Met Ser Asn His Phe Glu Cys Lys Cys Asn Asp
126   35         40          45
128 Gly Phe Val Met Ala Asn Glu Asn Thr Cys Glu Glu Lys Arg Asp Cys
129   50         55          60
131 Thr Asn Pro Gln Asn Val Asn Lys Asn Cys Gly Asp Tyr Ala Val Cys

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132	65	70	75	80
134	Ala Asn Thr Arg Met Asn Asp Glu Glu Arg Ala Leu Arg Cys Gly Cys			
135		85	90	95
137	Ile Leu Gly Tyr Thr Val Met Asn Glu Val Cys Thr Pro Asn Lys Cys			
138		100	105	110
140	Asn Gly Val Leu Cys Gly Lys Gly Lys Cys Ile Leu Asp Pro Ala Asn			
141		115	120	125
143	Val Asn Ser Thr Met Cys Ser Cys Asn Ile Gly Thr Thr Leu Asp Glu			
144		130	135	140
146	Ser Lys Lys Cys Gly Lys Pro Gly Lys Thr Glu Cys Thr Leu Lys Cys			
147		145	150	155
149	Lys Ala Asn Glu Glu Cys Lys Glu Thr Gln Asn Tyr Tyr Lys Cys Val			
150		165	170	175
152	Ala Lys Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly			
153		180	185	190
155	Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Asp			
156		195	200	205
158	Thr Gly Ala Ala Tyr Ser Leu Met Asn Gly Ser Ala Val Ile Ser Ile			
159		210	215	220
161	Leu Leu Val Phe Ala Phe Phe Met Met Ser Leu Val			
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165	<210> SEQ ID NO: 3			
166	<211> LENGTH: 995			
167	<212> TYPE: DNA			
168	<213> ORGANISM: Plasmodium vivax			
170	<220> FEATURE:			
171	<221> NAME/KEY: CDS			
172	<222> LOCATION: (255)..(914)			
173	<223> OTHER INFORMATION: Pvs25			
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176	ctgactttcg tttcacagca ctgattttt tgttcgaccg ctcaattcgc cacttgccat 60			
178	tttcgattgt ttgctgttt gctttttgc ttattcgccc gttttccgc ttgcccgttc 120			
180	gcccgctcca caacgcgccc ctgcaaagt tgccaccac cgaccacaaa aacttattca 180			
182	ccaccatccg agcggaaagg aacgcgcgc actgtgctgc ctacctcccc gaataacaac 240			
184	tccacttagc caaa atg aac tcc tac tac agc ctc ttc gtt ttt ttc ctc 290			
185	Met Asn Ser Tyr Tyr Ser Leu Phe Val Phe Phe Leu			
186		1	5	10
188	gtc caa att gcg cta aag tat agc aag gca gcc gtc acg gta gac acc 338			
189	Val Gln Ile Ala Leu Lys Tyr Ser Lys Ala Ala Val Thr Val Asp Thr			
190		15	20	25
192	ata tgc aaa aat gga cag ctg gtt caa atg agt aac cac ttt aag tgt 386			
193	Ile Cys Lys Asn Gly Gln Leu Val Gln Met Ser Asn His Phe Lys Cys			
194		30	35	40
196	atg tgt aac gaa ggg ctg gtg cac ctt tcc gaa aat aca tgt gaa gaa 434			
197	Met Cys Asn Glu Gly Leu Val His Leu Ser Glu Asn Thr Cys Glu Glu			
198		45	50	55
200	aaa aat gaa tgc aag aaa gaa acc cta ggc aaa gca tgc ggg gaa ttt 482			
201	Lys Asn Glu Cys Lys Lys Glu Thr Leu Gly Lys Ala Cys Gly Glu Phe			
202		65	70	75

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204 ggc cag tgt ata gaa aac cca gac cca gca cag gta aac atg tac aaa	530
205 Gly Gln Cys Ile Glu Asn Pro Asp Pro Ala Gln Val Asn Met Tyr Lys	
206 80 85 90	
208 tgt ggt tgc att gag ggc tac act ttg aag gaa gac act tgt gtg ctt	578
209 Cys Gly Cys Ile Glu Gly Tyr Thr Leu Lys Glu Asp Thr Cys Val Leu	
210 95 100 105	
212 gat gta tgt caa tac aaa aat tgt gga gaa agt ggc gaa tgc att gtt	626
213 Asp Val Cys Gln Tyr Lys Asn Cys Gly Glu Ser Gly Glu Cys Ile Val	
214 110 115 120	
216 gag tac ctc tcg gaa atc caa agt gca ggt tgc tca tgt gct att ggc	674
217 Glu Tyr Leu Ser Glu Ile Gln Ser Ala Gly Cys Ser Cys Ala Ile Gly	
218 125 130 135 140	
220 aaa gtc ccc aat cca gaa gat gag aaa aaa tgt acc aaa acg gga gaa	722
221 Lys Val Pro Asn Pro Glu Asp Glu Lys Lys Cys Thr Lys Thr Gly Glu	
222 145 150 155	
224 act gct tgt caa ttg aaa tgt aac aca gat aat gaa gtc tgc aaa aat	770
225 Thr Ala Cys Gln Leu Lys Cys Asn Thr Asp Asn Glu Val Cys Lys Asn	
226 160 165 170	
228 gtt gaa gga gtt tac aag tgc cag tgt atg gaa ggc ttt acg ttc gac	818
229 Val Glu Gly Val Tyr Lys Cys Gln Cys Met Glu Gly Phe Thr Phe Asp	
230 175 180 185	
232 aaa gag aaa aat gta tgc ctt tcc tat tct gta ttt aac atc cta aac	866
233 Lys Glu Lys Asn Val Cys Leu Ser Tyr Ser Val Phe Asn Ile Leu Asn	
234 190 195 200	
236 tac tcc ctc ttc ttt atc atc ctg ctt gtc ctt tcg tac gtc ata	911
237 Tyr Ser Leu Phe Phe Ile Ile Leu Leu Val Leu Ser Tyr Val Ile	
238 205 210 215	
240 taagtgcgaa acttgcgcag ctaaggcagcg caaatttttt aagttaaaaat acttttcttt	971
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245 <210> SEQ ID NO: 4	
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247 <212> TYPE: PRT	
248 <213> ORGANISM: Plasmodium vivax	
250 <400> SEQUENCE: 4	
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254 Leu Lys Tyr Ser Lys Ala Ala Val Thr Val Asp Thr Ile Cys Lys Asn	
255 20 25 30	
257 Gly Gln Leu Val Gln Met Ser Asn His Phe Lys Cys Met Cys Asn Glu	
258 35 40 45	
260 Gly Leu Val His Leu Ser Glu Asn Thr Cys Glu Glu Lys Asn Glu Cys	
261 50 55 60	
263 Lys Lys Glu Thr Leu Gly Lys Ala Cys Gly Glu Phe Gly Gln Cys Ile	
264 65 70 75 80	
266 Glu Asn Pro Asp Pro Ala Gln Val Asn Met Tyr Lys Cys Gly Cys Ile	
267 85 90 95	
269 Glu Gly Tyr Thr Leu Lys Glu Asp Thr Cys Val Leu Asp Val Cys Gln	
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272 Tyr Lys Asn Cys Gly Glu Ser Gly Glu Cys Ile Val Glu Tyr Leu Ser	

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273      115          120          125
275 Glu Ile Gln Ser Ala Gly Cys Ser Cys Ala Ile Gly Lys Val Pro Asn
276      130          135          140
278 Pro Glu Asp Glu Lys Lys Cys Thr Lys Thr Gly Glu Thr Ala Cys Gln
279      145          150          155          160
281 Leu Lys Cys Asn Thr Asp Asn Glu Val Cys Lys Asn Val Glu Gly Val
282          165          170          175
284 Tyr Lys Cys Gln Cys Met Glu Gly Phe Thr Phe Asp Lys Glu Lys Asn
285          180          185          190
287 Val Cys Leu Ser Tyr Ser Val Phe Asn Ile Leu Asn Tyr Ser Leu Phe
288          195          200          205
290 Phe Ile Ile Leu Leu Val Leu Ser Tyr Val Ile
291          210          215
294 <210> SEQ ID NO: 5
295 <211> LENGTH: 377
296 <212> TYPE: PRT
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence:Pvs25-Pvs28
301     fusion protein
303 <400> SEQUENCE: 5
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305      1           5           10          15
307 Ser Asn His Phe Lys Cys Met Cys Asn Glu Gly Leu Val His Leu Ser
308          20          25          30
310 Glu Asn Thr Cys Glu Glu Lys Asn Glu Cys Lys Lys Glu Thr Leu Gly
311          35          40          45
313 Lys Ala Cys Gly Glu Phe Gly Gln Cys Ile Glu Asn Pro Asp Pro Ala
314          50          55          60
316 Gln Val Asn Met Tyr Lys Cys Gly Cys Ile Glu Gly Tyr Thr Leu Lys
317          65          70          75          80
319 Glu Asp Thr Cys Val Leu Asp Val Cys Gln Tyr Lys Asn Cys Gly Glu
320          85          90          95
322 Ser Gly Glu Cys Ile Val Glu Tyr Leu Ser Glu Ile Gln Ser Ala Gly
323          100         105         110
325 Cys Ser Cys Ala Ile Gly Lys Val Pro Asn Pro Glu Asp Glu Lys Lys
326          115         120         125
328 Cys Thr Lys Thr Gly Glu Thr Ala Cys Gln Leu Lys Cys Asn Thr Asp
329          130         135         140
331 Asn Glu Val Cys Lys Asn Val Glu Gly Val Tyr Lys Cys Gln Cys Met
332          145         150         155          160
334 Glu Gly Phe Thr Phe Asp Lys Glu Lys Asn Val Cys Leu Ser Gly Gly
335          165         170         175
337 Gly Pro Gly Gly Ala Lys Val Thr Ala Glu Thr Gln Cys Lys Asn
338          180         185         190
340 Gly Tyr Val Val Gln Met Ser Asn His Phe Glu Cys Lys Cys Asn Asp
341          195         200         205
343 Gly Phe Val Met Ala Asn Glu Asn Thr Cys Glu Glu Lys Arg Asp Cys
344          210         215         220

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**VERIFICATION SUMMARY**

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Input Set : A:\Nih342-1.app

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date